

the extracellular portion of human CD40L

<300>

<301> Spriggs, Melanie K.
Armitage, Richard J.
Strockbine, L
Clifford, K N.
Macduff, B M.
Sato, T A.
Maliszewski, C R.
Fanslow, William C.

<302> Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin E secretion.

<303> J. Exp. Med.

<304> 176

<305> 6

<306> 1543-1550

<307> 1992

<313> 801 TO 1600

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<301> Motwani, M
White, R A.

<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.

<303> J. Immunol.

<304> 155

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<306> 5671-5677

<307> 1995

<313> 32 TO 800

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100

Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
10 15 20

agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt
148

Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga

196

Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg
244

Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
60 65 70

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292

Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta
340

Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa
388

Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt
436

Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg
484

Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga
532

Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
155 160 165

ggt gcc cct ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga
580

Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc
628

Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
185 190 195

cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa

676

Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200 205 210 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag
724

Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
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gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat
772

Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
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cag aaa gct gca ttg ttc cct gat ggc cat aga agg ttg gac aag ata
820

Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Ile
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gaa gat gaa agg aat ctt cat gaa gat ttt gta ttc atg aaa acg ata
868

Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr Ile
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Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu
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gag att aaa agc cag ttt gaa ggc ttt gtg aag gat ata atg tta aac
964

Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu Asn
300 305 310

aaa gag gag acg aag aaa gaa aac agc ttt gaa atg caa aaa ggt gat
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1060

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330 335 340

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1108

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345 350 355

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1156

Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg
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1252

Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser
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1300

Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser
410 415 420

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1348

Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly Val Phe
425 430 435

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1396

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1444

Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
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<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
surfactant protein D (without the CRD) fused to
the extracellular portion of human CD40L

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Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
35 40 45

Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
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Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
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Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
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Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp
260 265 270

Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
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Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
305 310 315 320

Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
325 330 335

Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
340 345 350

Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
355 360 365

Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
370 375 380

Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
385 390 395 400

Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
405 410 415

Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
420 425 430

Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
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protein D

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<223> Signal peptide from murine surfactant protein D

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<222> (32)..(800)

<223> Murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

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<222> (801)..(1534)

<223> Murine RANKL/TRANCE extracellular region, including stalk

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<301> Motwani, M

White, R A.

Guo, N

Dowler, L L.

Tauber, A I.

Motwani, M

<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.

<303> J. Immunol.

<304> 155

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<306> 5671-5677

<307> 1995

<313> 32 TO 800

<300>

<301> Anderson, D M.

Maraskovsky, E

Billingsley, W L.

Dougall, W C.

<302> A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.

<303> Nature

<304> 390

<305> 6656
<306> 175-179
<307> 1997
<313> 801 TO 1534

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Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
10 15 20

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Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga
196
Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg
244
Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
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Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
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Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa
388
Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggc ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt
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Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

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Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

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Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
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Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly
170 175 180

cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc
628
Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
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676
Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
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Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
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Gln Lys Ala Ala Leu Phe Pro Asp Gly Arg Ala Gln Met Asp Pro Asn
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Arg Ile Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu
265 270 275

cat gaa aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca
916
His Glu Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr
280 285 290 295

cta cct gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg
964
Leu Pro Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val
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cag aag gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct
1012
Gln Lys Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala
315 320 325

cca gct atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag
1060
Pro Ala Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys
330 335 340

cct gag gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc
1108
Pro Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile
345 350 355

cca tcg ggt tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga
1156
Pro Ser Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg
360 365 370 375

ggc tgg gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg
1204
Gly Trp Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg
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gtt aac caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg
1252
Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
395 400 405

cat cat gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg
1300
His His Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met
410 415 420

gtg tat gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg
1348
Val Tyr Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu
425 430 435

atg aaa gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac
1396
Met Lys Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His
440 445 450 455

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1444

Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu
460 465 470

gaa att agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa
1492

Glu Ile Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
475 480 485

gat gcg acg tac ttt ggg gct ttc aaa gtt cag gac ata gac
1534

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35 40 45

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50 55 60

Pro Gly Leu Pro Gly Pro Met Gly Leu Ser Gly Leu Gln Gly Pro Thr
65 70 75 80

Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
85 90 95

Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
100 105 110

Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
115 120 125

Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly

130 135 140

Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
145 150 155 160

Thr Gly Pro Lys Gly Glu Arg Gly Ala Pro Gly Val Gln Gly Ala Pro
165 170 175

Gly Asn Ala Gly Ala Ala Gly Pro Ala Gly Pro Ala Gly Pro Gln Gly
180 185 190

Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
195 200 205

Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
210 215 220

Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
225 230 235 240

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His Cys
260 265 270

Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp Ser
275 280 285

Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met Lys
290 295 300

Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val Gly
305 310 315 320

Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp Leu
325 330 335

Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His Leu
340 345 350

Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr Leu
355 360 365

Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met Thr
370 375 380

Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr Leu
385 390 395 400

Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val Pro
405 410 415

Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile Lys
420 425 430

Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn Trp
435 440 445

Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly Phe
450 455 460

Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn Pro
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Val Gln Asp Ile Asp
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<212> DNA

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<223> Description of Artificial Sequence: Murine
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extracellular domain of murine CD40 ligand

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<222> (7)..(31)

<223> 5' UTR from rat surfactant protein D

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<222> (32)..(88)

<223> Signal peptide from murine surfactant protein D

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<221> CDS

<222> (32)..(1441)

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<222> (88)..(799)

<223> Mature murine surfactant protein D including hub region, collagenous portion, and neck, but excluding carbohydrate recognition domain (CRD)

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<222> (800)..(1441)

<223> Murine CD40 ligand extracellular region, including stalk

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<301> Motwani, M

White, R A.

Guo, N

Dowler, L L.

Tauber, A I.

Motwani, M

<302> Mouse surfactant protein-D. cDNA cloning, characterization, and gene localization to chromosome 14.

<303> J. Immunol.

<304> 155

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Fanslow, W

Sato, T A.

Clifford, K N.

<302> Molecular and biological characterization of a murine ligand for CD40

<303> Nature

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<305> 6373

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<307> 1992

<313> 801 TO 1441

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100

Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys

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agc ctc tcg cag aga tca gta ccc aac acc acc tgc acc cta gtc atg tgt
148

Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
25 30 35

agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga
196

Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
40 45 50 55

gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg
244

Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
60 65 70

ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga
292

Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
75 80 85

gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta
340

Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
90 95 100

agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa
388

Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
105 110 115

ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt
436

Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
120 125 130 135

cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg
484

Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
140 145 150

caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga
532

Gln Gly Ser Thr Gly Ala Lys Gly Ser Thr Gly Pro Lys Gly Glu Arg
155 160 165

ggc ccc ggt gtg caa gga gcc cca ggg aat gct gga gca gca gga
580

Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly

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cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc
628

Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro
185 190 195

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676

Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys
200 205 210 215

ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag
724

Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu
220 225 230

gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat
772

Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr
235 240 245

cag aaa gct gca ttg ttc cct gat ggc cat aga aga ttg gat aag gtc
820

Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Val
250 255 260

gaa gag gaa gta aac ctt cat gaa gat ttt gta ttc ata aaa aag cta
868

Glu Glu Glu Val Asn Leu His Glu Asp Phe Val Phe Ile Lys Lys Leu
265 270 275

aag aga tgc aac aaa gga gaa gga tct tta tcc ttg ctg aac tgt gag
916

Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser Leu Leu Asn Cys Glu
280 285 290 295

gag atg aga agg caa ttt gaa gac ctt gtc aag gat ata acg tta aac
964

Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys Asp Ile Thr Leu Asn
300 305 310

aaa gaa gag aaa aaa gaa aac agc ttt gaa atg caa aga ggt gat gag
1012

Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met Gln Arg Gly Asp Glu
315 320 325

gat cct caa att gca gca cac gtt gta agc gaa gcc aac agt aat gca
1060

Asp Pro Gln Ile Ala Ala His Val Val Ser Glu Ala Asn Ser Asn Ala

330

335

340

gca tcc gtt cta cag tgg gcc aag aaa gga tat tat acc atg aaa agc
1108

Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr Tyr Thr Met Lys Ser
345 350 355

aac ttg gta atg ctt gaa aat ggg aaa cag ctg acg gtt aaa aga gaa
1156

Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Glu
360 365 370 375

gga ctc tat tat gtc tac act caa gtc acc ttc tgc tct aat cgg gag
1204

Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe Cys Ser Asn Arg Glu
380 385 390

cct tcg agt caa cgc cca ttc atc gtc ggc ctc tgg ctg aag ccc agc
1252

Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu Trp Leu Lys Pro Ser
395 400 405

att gga tct gag aga atc tta ctc aag gcg gca aat acc cac agt tcc
1300

Ile Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala Asn Thr His Ser Ser
410 415 420

tcc cag ctt tgc gag cag cag tct gtt cac ttg ggc gga gtg ttt gaa
1348

Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu Gly Gly Val Phe Glu
425 430 435

tta caa gct ggt gct tct gtg ttt gtc aac gtg act gaa gca agc caa
1396

Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln
440 445 450 455

gtg atc cac aga gtt ggc ttc tca tct ttt ggc tta ctc aaa ctc
1441

Val Ile His Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu
460 465 470

tgaacagtgc gctgtcctag gctgcagcag ggtacc
1477

<210> 6

<211> 470

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Murine
surfactant protein D (except CRD) fused to the
extracellular domain of murine CD40 ligand

<400> 6

Met	Leu	Pro	Phe	Leu	Ser	Met	Leu	Val	Leu	Leu	Val	Gln	Pro	Leu	Gly
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				20				25				30			
Thr	Cys	Thr	Leu	Val	Met	Cys	Ser	Pro	Thr	Glu	Asn	Gly	Leu	Pro	Gly
					35			40				45			
Arg	Asp	Gly	Arg	Asp	Gly	Arg	Glu	Gly	Pro	Arg	Gly	Glu	Lys	Gly	Asp
	50					55				60					
Pro	Gly	Leu	Pro	Gly	Pro	Met	Gly	Leu	Ser	Gly	Leu	Gln	Gly	Pro	Thr
					65		70			75				80	
Gly	Pro	Val	Gly	Pro	Lys	Gly	Glu	Asn	Gly	Ser	Ala	Gly	Glu	Pro	Gly
					85				90				95		
Pro	Lys	Gly	Glu	Arg	Gly	Leu	Ser	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Ile
					100			105				110			
Pro	Gly	Pro	Ala	Gly	Lys	Glu	Gly	Pro	Ser	Gly	Lys	Gln	Gly	Asn	Ile
		115				120						125			
Gly	Pro	Gln	Gly	Lys	Pro	Gly	Pro	Lys	Gly	Glu	Ala	Gly	Pro	Lys	Gly
		130				135				140					
Glu	Val	Gly	Ala	Pro	Gly	Met	Gln	Gly	Ser	Thr	Gly	Ala	Lys	Gly	Ser
	145					150				155				160	
Thr	Gly	Pro	Lys	Gly	Glu	Arg	Gly	Ala	Pro	Gly	Val	Gln	Gly	Ala	Pro
					165				170				175		
Gly	Asn	Ala	Gly	Ala	Ala	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Gln	Gly
					180			185				190			
Ala	Pro	Gly	Ser	Arg	Gly	Pro	Pro	Gly	Leu	Lys	Gly	Asp	Arg	Gly	Val
						195		200				205			
Pro	Gly	Asp	Arg	Gly	Ile	Lys	Gly	Glu	Ser	Gly	Leu	Pro	Asp	Ser	Ala
					210		215				220				
Ala	Leu	Arg	Gln	Gln	Met	Glu	Ala	Leu	Lys	Gly	Lys	Leu	Gln	Arg	Leu
					225		230				235			240	

Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
245 250 255

His Arg Arg Leu Asp Lys Val Glu Glu Val Asn Leu His Glu Asp
260 265 270

Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser
275 280 285

Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu
290 295 300

Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe
305 310 315 320

Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val
325 330 335

Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys
340 345 350

Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys
355 360 365

Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val
370 375 380

Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val
385 390 395 400

Gly Leu Trp Leu Lys Pro Ser Ile Gly Ser Glu Arg Ile Leu Leu Lys
405 410 415

Ala Ala Asn Thr His Ser Ser Gln Leu Cys Glu Gln Gln Ser Val
420 425 430

His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val
435 440 445

Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser
450 455 460

Phe Gly Leu Leu Lys Leu
465 470